

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/088,859A

Source: 1FW16

Date Processed by STIC: 2/28/06

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IFW16

RAW SEQUENCE LISTING

DATE: 07/28/2006

PATENT APPLICATION: US/10/088,859A

TIME: 14:32:52

Input Set : A:\Revised Sequence Listing filed 2006-07-26.txt

Output Set: N:\CRF4\07282006\J088859A.raw

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3 <110> APPLICANT: KATO, Seishi
4     NAGATA, Naoki
5     FUJIMURA, Naoko
6     KOBAYASHI, Midori
7     ITO, Koichi
8     ISHIZUKA, Yoshiko
10 <120> TITLE OF INVENTION: A Method For Producing An Antibody By Gene Immunization
12 <130> FILE REFERENCE: 2002_0400A
14 <140> CURRENT APPLICATION NUMBER: 10/088,859A
15 <141> CURRENT FILING DATE: 2002-05-29
17 <150> PRIOR APPLICATION NUMBER: PCT/JP01/06371
18 <151> PRIOR FILING DATE: 2001-07-24
20 <150> PRIOR APPLICATION NUMBER: PCT2000-222743
21 <151> PRIOR FILING DATE: 2000-07-24
23 <150> PRIOR APPLICATION NUMBER: JP2000-254407
24 <151> PRIOR FILING DATE: 2000-08-24
26 <160> NUMBER OF SEQ ID NOS: 18
28 <170> SOFTWARE: PatentIn version 3.3
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 697
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (151)..(600)
40 <400> SEQUENCE: 1
41 tataacctcta gtttggagct gtgctgtaaa aacaagagta acatttttat attaaagtta      60
43 aataaaagtta caactttgaa gagagtttct gcaagacatg acacaaaagct gctagcagaa      120
45 aatcaaaaacg ctgattaaaa gaagcacggt atg atg acc aaa cat aaa aag tgt      174
46                                     Met Met Thr Lys His Lys Lys Cys
47                                     1           5
49 ttt ata att gtt ggt gtt tta ata aca act aat att att act ctg ata      222
50 Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile
51     10           15           20
53 gtt aaa cta act cga gat tct cag agt tta tgc ccc tat gat tgg att      270
54 Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile
55 25           30           35           40
57 ggt ttc caa aac aaa tgc tat tat ttc tct aaa gaa gaa gga gat tgg      318
58 Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Glu Gly Asp Trp
59           45           50           55
61 aat tca agt aaa tac aac tgt tcc act caa cat gcc gac cta act ata      366
62 Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile
63           60           65           70

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65 att gac aac ata gaa gaa atg aat ttt ctt agg cgg tat aaa tgc agt      414
66 Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser
67      75      80      85
69 tct gat cac tgg att gga ctg aag atg gca aaa aat cga aca gga caa      462
70 Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln
71      90      95      100
73 tgg gta gat gga gct aca ttt acc aaa tcg ttt ggc atg aga ggg agt      510
74 Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser
75 105      110      115      120
77 gaa gga tgt gcc tac ctc agc gat gat ggt gca gca aca gct aga tgt      558
78 Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys
79      125      130      135
81 tac acc gaa aga aaa tgg att tgc agg aaa aga ata cac taa      600
82 Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His
83      140      145
85 gttaatgtct aagataatgg ggaaaataga aaataacatt attaagtgtgta aaaccagcaa      660
87 agtacttttt taattaaaca aagttcgagt tttgtac      697
90 <210> SEQ ID NO: 2
91 <211> LENGTH: 149
92 <212> TYPE: PRT
93 <213> ORGANISM: Homo sapiens
95 <400> SEQUENCE: 2
97 Met Met Thr Lys His Lys Lys Cys Phe Ile Ile Val Gly Val Leu Ile
98 1      5      10      15
101 Thr Thr Asn Ile Ile Thr Leu Ile Val Lys Leu Thr Arg Asp Ser Gln
102      20      25      30
105 Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr
106      35      40      45
109 Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser
110      50      55      60
113 Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn
114 65      70      75      80
117 Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys
118      85      90      95
121 Met Ala Lys Asn Arg Thr Gly Gln Trp Val Asp Gly Ala Thr Phe Thr
122      100      105      110
125 Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp
126      115      120      125
129 Asp Gly Ala Ala Thr Ala Arg Cys Tyr Thr Glu Arg Lys Trp Ile Cys
130      130      135      140
133 Arg Lys Arg Ile His
134 145
137 <210> SEQ ID NO: 3
138 <211> LENGTH: 548
139 <212> TYPE: DNA
140 <213> ORGANISM: Homo sapiens
143 <220> FEATURE:
144 <221> NAME/KEY: CDS
145 <222> LOCATION: (30)..(503)

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147 <400> SEQUENCE: 3
148 cttattgctg gcggcctgag gagcccatc atg gcg acg ccc cct aag cgg cgg      53
149                               Met Ala Thr Pro Pro Lys Arg Arg
150                               1                5
152 gcg gtg gag gcc acg ggg gag aaa gtg ctg cgc tac gag acc ttc atc      101
153 Ala Val Glu Ala Thr Gly Glu Lys Val Leu Arg Tyr Glu Thr Phe Ile
154    10                15                20
156 agt gac gtg ctg cag cgg gac ttg cga aag gtg ctg gac cat cga gac      149
157 Ser Asp Val Leu Gln Arg Asp Leu Arg Lys Val Leu Asp His Arg Asp
158 25                30                35                40
160 aag gta tat gag cag ctg gcc aaa tac ctt caa ctg aga aat gtc att      197
161 Lys Val Tyr Glu Gln Leu Ala Lys Tyr Leu Gln Leu Arg Asn Val Ile
162                               45                50                55
164 gag cga ctc cag gaa gct aag cac tcg gag tta tat atg cag gtg gat      245
165 Glu Arg Leu Gln Glu Ala Lys His Ser Glu Leu Tyr Met Gln Val Asp
166                               60                65                70
168 ttg ggc tgt aac ttc ttc gtt gac aca gtg gtc cca gat act tca cgc      293
169 Leu Gly Cys Asn Phe Phe Val Asp Thr Val Val Pro Asp Thr Ser Arg
170    75                80                85
172 atc tat gtg gcc ctg gga tat ggt ttt ttc ctg gag ttg aca ctg gca      341
173 Ile Tyr Val Ala Leu Gly Tyr Gly Phe Phe Leu Glu Leu Thr Leu Ala
174    90                95                100
176 gaa gct ctc aag ttc att gat cgt aag agc tct ctc ctc aca gag ctc      389
177 Glu Ala Leu Lys Phe Ile Asp Arg Lys Ser Ser Leu Leu Thr Glu Leu
178 105                110                115                120
180 agc aac agc ctc acc aag gac tcc atg aat atc aaa gcc cat atc cac      437
181 Ser Asn Ser Leu Thr Lys Asp Ser Met Asn Ile Lys Ala His Ile His
182                               125                130                135
184 atg ttg cta gag ggg ctt aga gaa cta caa ggc ctg cag aat ttc cca      485
185 Met Leu Leu Glu Gly Leu Arg Glu Leu Gln Gly Leu Gln Asn Phe Pro
186                               140                145                150
188 gag aag cct cac cat tga cttcttcccc ccatacctcag acattaaaga      533
189 Glu Lys Pro His His
190                               155
192 gcctgaatgc ctttg      548
195 <210> SEQ ID NO: 4
196 <211> LENGTH: 157
197 <212> TYPE: PRT
198 <213> ORGANISM: Homo sapiens
200 <400> SEQUENCE: 4
202 Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu Ala Thr Gly Glu Lys
203 1                5                10                15
206 Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
207    20                25                30
210 Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys
211    35                40                45
214 Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
215    50                55                60
218 Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp

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219 65          70          75          80
222 Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
223          85          90          95
226 Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
227          100          105          110
230 Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
231          115          120          125
234 Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
235          130          135          140
238 Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
239 145          150          155
242 <210> SEQ ID NO: 5
243 <211> LENGTH: 30
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Oligonucleotide
250 <400> SEQUENCE: 5
251 ccgatatct catggcgacg cccctaagc. 30
254 <210> SEQ ID NO: 6
255 <211> LENGTH: 30
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Oligonucleotide
262 <400> SEQUENCE: 6
263 ccgatatct caatggtgag gcttctctgg 30
266 <210> SEQ ID NO: 7
267 <211> LENGTH: 28
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Oligonucleotide
274 <400> SEQUENCE: 7
275 cccgaattca tggcgacgcc ccctaagc 28
278 <210> SEQ ID NO: 8
279 <211> LENGTH: 32
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Oligonucleotide
286 <400> SEQUENCE: 8
287 cccgtcgacg catggtgagg cttctctggg aa 32
290 <210> SEQ ID NO: 9
291 <211> LENGTH: 1643
292 <212> TYPE: DNA
293 <213> ORGANISM: Homo sapiens
296 <220> FEATURE:
297 <221> NAME/KEY: CDS

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298 <222> LOCATION: (25)..(915)
300 <400> SEQUENCE: 9
301 aacatctggg gacagcggga aaac atg agt gac tcc aag gaa cca agg gtg      51
302                               Met Ser Asp Ser Lys Glu Pro Arg Val
303                               1           5
305 cag cag ctg ggc ctc ctg ggg tgt ctt ggc cat ggc gcc ctg gtg ctg      99
306 Gln Gln Leu Gly Leu Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu
307 10           15           20           25
309 caa ctc ctc tcc ttc atg ctc ttg gct ggg gtc ctg gtg gcc atc ctt      147
310 Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu
311           30           35           40
313 gtc caa gtg tcc aag gtc ccc agc tcc cta agt cag gaa caa tcc gag      195
314 Val Gln Val Ser Lys Val Pro Ser Ser Leu Ser Gln Glu Gln Ser Glu
315           45           50           55
317 caa gac gca atc tac cag aac ctg acc cag ctt aaa gct gca gtg ggt      243
318 Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly
319           60           65           70
321 gag ctc tca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc      291
322 Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
323           75           80           85
325 cag ctg aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag      339
326 Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
327 90           95           100           105
329 gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg      387
330 Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu
331           110           115           120
333 cca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc cgg ctg      435
334 Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
335           125           130           135
337 aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc      483
338 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile
339           140           145           150
341 tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg cca gag      531
342 Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
343           155           160           165
345 aaa tcc aag ctg cag gag atc tac cag gag ctg acg gag ctg aag gct      579
346 Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Glu Leu Lys Ala
347 170           175           180           185
349 gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc tac cag      627
350 Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln
351           190           195           200
353 gag ctg acc cag ctg aag gct gca gtg ggt gag ttg cca gac cag tcc      675
354 Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser
355           205           210           215
357 aag cag cag caa atc tat caa gaa ctg acc gat ttg aag act gca ttt      723
358 Lys Gln Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe
359           220           225           230
361 gaa cgc ctg tgc cgc cac tgt ccc aag gac tgg aca ttc ttc caa gga      771
362 Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,14,15,16,17,18

VERIFICATION SUMMARY

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